

Figure 1

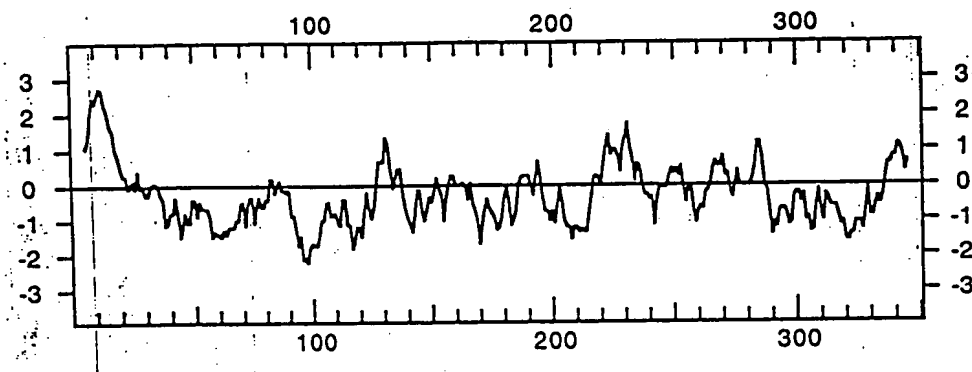
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ATG CAG CGG CTT GGG GCC ACC CTG CTG TGC		67
L L L A A A V P T A P A P A P T A T S A		30
CTG CTG CTG GCG GCG GCG GTC CCC ACG GCC CCC GCG CCC GCT CCG ACG GCG ACC TCG GCT		127
P V K P G P A L S Y P Q E E A T L N E M		50
CCA GTC AAG CCC GGC CCG GCT CTC AGC TAC CCG CAG GAG GAG GCC ACC CTC AAT GAG ATG		187
F R E V E E L M E D T Q H K L R S A V E		70
TTC CGC GAG GTT GAG GAA CTG ATG GAG GAC ACG CAG CAC AAA TTG CGC AGC GCG GTG GAA		247
E M E A E E A A A K A S S E V N L A N L		30
GAG ATG GAG GCA GAA GAA GCT GCT GCT AAA GCA TCA TCA GAA GTG AAC CTG GCA AAC TTA		307
P P S Y H N E T N T D T N V G N N T I H		110
CCT CCC AGC TAT CAC AAT GAG ACC AAC ACA GAC ACG AAC GTT GGA AAT AAT ACC ATC CAT		367
V H R E I H K I T N N Q T G Q M V F S E		130
GTG CAC CGA GAA ATT CAC AAG ATA ACC AAC AAC CAG ACT GGA CAA ATG GTC TTT TCA GAG		427
T V I T S V G D E E G R R S H E C I I D		150
ACA GTT ATC ACA TCT GTG GGA GAC GAA GAA GGC AGA AGG AGC CAC GAG TGC ATC ATC GAC		487
E D C G P S M Y C Q F A S F Q Y T C Q P		170
GAG GAC TGT GGG CCC AGC ATG TAC TGC CAG TTT GCC AGC TTC CAG TAC ACC TGC CAG CCA		547
C R G Q R M L C T R D S E C C G D Q L C		190
TGC CGG GGC CAG AGG ATG CTC TGC ACC CGG GAC AGT GAG TGC TGT GGA GAC CAG CTG TGT		607
V W G H C T K M A T R G S N G T I C D N		210
GTC TGG GGT CAC TGC ACC AAA ATG GCC ACC AGG GGC AGC AAT GGG ACC ATC TGT GAC AAC		667
Q R D C Q P G L C C A F Q R G L L F P V		230
CAG AGG GAC TGC CAG CCG GGG CTG TGC TGT GCC TTC CAG AGA GGC CTG CTG TTC CCT GTG		727
C T P L P V E G E L C H D P A S R L L D		250
TGC ACA CCC CTG CCC GTG GAG GGC GAG CTT TGC CAT GAC CCC GCC AGC CGG CTT CTG GAC		787
L I T W E L E P D G A L D R C P C A S G		270
CTC ATC ACC TGG GAG CTA GAG CCT GAT GGA GCC TTG GAC CGA TGC CCT TGT GCC AGT GGC		847
L L C Q P H S H S L V Y V C K P T F V G		290
CTC CTC TGC CAG CCC CAC AGC CAC AGC CTG GTG TAT GTG TGC AAG CCG ACC TTC GTG GGG		907
S R D Q D G E I L L P R E V P D E Y E V		310
AGC CGT GAC CAA GAT GGG GAG ATC CTG CTG CCC AGA GAG GTC CCC GAT GAG TAT GAA GTT		967
G S F M E E V R Q E L E D L E R S L T E		330
GGC AGC TTC ATG GAG GAG GTG CGC CAG GAG CTG GAG GAC CTG GAG AGG AGC CTG ACT GAA		1027
E M A L R E P A A A A A A L L G R E E I		350
GAG ATG GCG CTG AGG GAG CCT GCG GCT GCC GCC GCT GCA CTG CTG GGA AGG GAA GAG ATT		1087
•		351
TAG		1090
ATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTATTTCCTCCAGTGTGTGCTTTAAGCGTGGGCTG		1169

00042393 041797

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00442898.041797

Figure 2



03042898.04.1797

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1  ..MORLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYQPQEEATLN 48
  ..  .|. :|| || .| ..|:..... :|  |.|.
1  MRRGEGPAPRRRWLLLLAVLAALCCAAAGSGRRRA.....ASLG 40

49  EMFREVEELMEDTQHKLRSERVEEEMAEAAAKASSEVNLANLPPSYHNET 98
  ||:||||.|||||||.||:|||||.:||  |||:..|||.||||.
41  EMLREVEALMEDTQHKLRNAVQEMEAELEGAKKLSEVNFENLPPTYHNES 90
  ||:|.:.||:|.:.||:|.:.||:|.:.||  :||||:||||: :. .|.|||

99  NTDTNVGNNTIHHVHREIHKITNNQTCQMVFSETVITSVGDEFGRGHEEI 148
  ||:|.:.||:|.:.||:|.:.||:|.:.||  :||||:||||: :. .|.|||
91  NTETRIGNKTVQTHQEKDVTDNRTGSTIFSETIITSIKGGENKRNHEEI 140

149  IDEDEGSPSMYQFASFQYTFQPERGQRMGLGTRDSEGGDQLEWVGHCTKM 198
  |||||.:.|||..|:|.|||:|.:.||  |||||.:.|||..|:|.|||
141  IDEDEGCTGKYQFSTFEYKQCPCKTQHTHCSRDEGGDQLEWVGECRKA 190

199  ATRGSNGTICDNQRDCQPGLCQAFQRGLLFPVCTPLPVEGELCHDPASRL 248
  ..|||.||||:|:|.|||  |||:|||||  |||..||
191  TSRGENGTICENQHDCNPGTCQAFQKELLFPVCTPLPEEGEPCHDPSNRL 240

249  LDLITWELEPDGALDRQPCASGLLCQPH.SHSLVYVCKPTFVGSRDQDGE 297
  |:|||||||.||:|  |||||:|  |||.|||.  ..|...|
241  LNLITWELEPDGVLERCPCASGLICQPOSSHSTTSVCELSSNETRKNEKE 290

298  .....ILLPREVPDEYEVGSFMEEVRQELEDLERSLTEEMALRE 336
  |:|::: .:|  |:|:|  |||  ||::: :.:.
291  DPLNMDEMPFISLIPRDILSDYEESSVIQEVKKE....SLEDQAGVKS 336

337  PAAAAAALLGREEI 350
  .:|.:.|:  :||
337  EHDPAHDLFLGDEI 350

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337 PAAAAAALLGREEI 350
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337 EHDPAHDLFLGDEI 350

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